

# SEQUENCE LISTING

<110> DeVico et al, Anthony

<120> VIRUS COAT PROTEIN/RECEPTOR CHIMERAS AND METHODS OF USE

<130> 4115-144 CIP

<160> 33

<170> PatentIn version 3.1

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<212> DNA

<213> Artificial Sequence

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<223> Synthesized construct

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Phe Cys Ala Ser Asp Arg Lys Ala Tyr Asp Thr Glu Val His Asn Val  
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Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Val  
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Glu Leu Lys Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met  
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Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu  
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Ile Arg Ser Ala Asn Phe Ala Asp Asn Ala Lys Val Ile Ile Val Gln  
 275 280 285

Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr  
 290 295 300

Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly  
 305 310 315 320

Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala  
 325 330 335

Lys Trp Asn Asp Thr Leu Asn Lys Ile Val Ile Lys Leu Arg Glu Gln  
 340 345 350

Phe Gly Asn Lys Thr Ile Val Phe Lys His Ser Ser Gly Gly Asp Pro  
 355 360 365

Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys  
 370 375 380

Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Asn Val Thr Glu Glu Ser  
 385 390 395 400

Asn Asn Thr Val Glu Asn Asn Thr Ile Thr Leu Pro Cys Arg Ile Lys  
 405 410 415

Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala Met Tyr Ala Pro  
 420 425 430

Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu  
 435 440 445

Leu Thr Arg Asp Gly Gly Pro Glu Asp Asn Lys Thr Glu Val Phe Arg  
 450 455 460

Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys  
 465 470 475 480

Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala  
 485 490 495

Lys Arg Arg Val Val Gln Arg Glu Lys Arg Gly Ser Ser Gly Gly Gly  
 500 505 510

Gly Ser Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ala Ala Ala Lys  
 515 520 525

Lys Val Val Leu Gly Lys Lys Gly Asp Thr Val Glu Leu Thr Cys Thr  
 530 535 540

Ala Ser Gln Lys Lys Ser Ile Gln Phe His Trp Lys Asn Ser Asn Gln  
 545 550 555 560

Ile Lys Ile Leu Gly Asn Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser  
 565 570 575

Lys Leu Asn Asp Arg Ala Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly  
 580 585 590

Asn Phe Pro Leu Ile Ile Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr  
 595 600 605

Tyr Ile Cys Glu Val Glu Asp Gln Lys Glu Glu Val Gln Leu Leu Val  
 610 615 620

Phe Gly Leu Thr Ala Asn Ser Asp Thr His Leu Leu Gln Gly Gln Ser  
 625 630 635 640

Leu Thr Leu Thr Leu Glu Ser Pro Pro Gly Ser Ser Pro Ser Val Gln  
 645 650 655

Cys Arg Ser Pro Arg Gly Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser  
660 665 670

Val Ser Gln Leu Glu Leu Gln Asp Ser Gly Thr Trp Thr Cys Thr Val  
675 680 685

Leu Gln Asn Gln Lys Lys Val Glu Phe Lys Ile Asp Ile Val Val Leu  
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Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Xaa Tyr Val Xaa Thr  
705 710 715 720

<210> 3  
<211> 2159  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthesized construct

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tcctgcctcg gaaacgccga ggagaagctg tgggtgaccg tgtactacgg cgtgcccgtg 120  
tggaaggagg ccaccaccac cctgttctgc gccagcgacc gcaaggccta cgacaccgag 180  
gtgcacaacg tgtggggccac ccacgcctgc gtgcccaccg accccaaccc ccaggaggtg 240  
gagctgaaga acgtgaccga gaacttcaac atgtggaaga acaacatggg ggagcagatg 300  
cacgaggaca tcatcagcct gtgggaccag agcctgaagc cctgctgtaa gctgaccccc 360  
ctgtgctgta ccctgaactg caccgacctg cgcaacgcc ccaacggcaa cgacaccaac 420  
accactagta gcagccgcgg catggtgggc ggcggcgaga tgaagaactg cagcttcaac 480  
atcaccacca acatccgcgg caaggtgcag aaggagtacg ccctgttcta caagctggac 540  
atcgcccca tcgacaacaa cagcaacaac cgctaccgcc tgatcagctg caacaccagc 600  
gtgatcacc aggcctgccc caaggtgagc ttogagccca tccccatcca ctactgcgcc 660  
cccgccggct tcgccatcct gaagtgcag gacaagaagt tcaacggcaa gggcccctgc 720  
accaacgtga gcaccgtgca gtgcacccac ggcacccgcc ccgtggtgag caccagctg 780  
ctgctgaacg gcagcctggc cgaggaggag gtggtgatcc gcagcgcaa cttcgccgac 840  
aacgccaagg tgatcatcgt gcagctgaac gagagcgtgg agatcaactg caccgcccc 900  
aacaacaaca cccgcaagtc catccacatc ggccccggcc gcgccttcta caccaccggc 960



Met Pro Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu Leu Gly  
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 Met Leu Val Ala Ser Cys Leu Gly Asn Ala Glu Glu Lys Leu Trp Val  
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 Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr Thr Leu  
 35 40 45  
  
 Phe Cys Ala Ser Asp Arg Lys Ala Tyr Asp Thr Glu Val His Asn Val  
 50 55 60  
  
 Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Val  
 65 70 75 80  
  
 Glu Leu Lys Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met  
 85 90 95  
  
 Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu  
 100 105 110  
  
 Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Thr  
 115 120 125  
  
 Asp Leu Arg Asn Ala Thr Asn Gly Asn Asp Thr Asn Thr Thr Ser Ser  
 130 135 140  
  
 Ser Arg Gly Met Val Gly Gly Gly Glu Met Lys Asn Cys Ser Phe Asn  
 145 150 155 160  
  
 Ile Thr Thr Asn Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Leu Phe  
 165 170 175  
  
 Tyr Lys Leu Asp Ile Ala Pro Ile Asp Asn Asn Ser Asn Asn Arg Tyr  
 180 185 190  
  
 Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys  
 195 200 205  
  
 Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe  
 210 215 220  
  
 Ala Ile Leu Lys Cys Lys Asp Lys Lys Phe Asn Gly Lys Gly Pro Cys



225		230		235		240
Thr Asn Val Ser	Thr Val Gln Cys	Thr His Gly Ile Arg	Pro Val Val			
	245	250	255			
Ser Thr Gln Leu	Leu Leu Asn Gly	Ser Leu Ala Glu	Glu Glu Val Val			
	260	265	270			
Ile Arg Ser Ala	Asn Phe Ala Asp	Asn Ala Lys Val	Ile Ile Val Gln			
	275	280	285			
Leu Asn Glu Ser	Val Glu Ile Asn Cys	Thr Arg Pro Asn	Asn Asn Asn Thr			
	290	295	300			
Arg Lys Ser Ile	His Ile Gly Pro Gly	Arg Ala Phe Tyr	Thr Thr Gly			
305	310	315	320			
Glu Ile Ile Gly	Asp Ile Arg Gln Ala	His Cys Asn Leu	Ser Arg Ala			
	325	330	335			
Lys Trp Asn Asp	Thr Leu Asn Lys	Ile Val Ile Lys	Leu Arg Glu Gln			
	340	345	350			
Phe Gly Asn Lys	Thr Ile Val Phe	Lys His Ser Ser	Gly Gly Asp Pro			
	355	360	365			
Glu Ile Val Thr	His Ser Phe Asn Cys	Gly Gly Glu Phe	Phe Tyr Cys			
	370	375	380			
Asn Ser Thr Gln	Leu Phe Asn Ser Thr	Trp Asn Val Thr	Glu Glu Ser			
	385	390	395	400		
Asn Asn Thr Val	Glu Asn Asn Thr	Ile Thr Leu Pro	Cys Arg Ile Lys			
	405	410	415			
Gln Ile Ile Asn	Met Trp Gln Glu Val	Gly Arg Ala Met	Tyr Ala Pro			
	420	425	430			
Pro Ile Arg Gly	Gln Ile Arg Cys Ser	Ser Asn Ile Thr	Gly Leu Leu			
	435	440	445			
Leu Thr Arg Asp	Gly Gly Pro Glu Asp	Asn Lys Thr Glu	Val Phe Arg			
	450	455	460			

Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys  
465 470 475 480

Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala  
485 490 495

Lys Arg Arg Val Val Gln Arg Glu Lys Thr Gly Ser Ser Gly Gly Gly  
500 505 510

Gly Ser Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ala Ala Ala Lys  
515 520 525

Lys Val Val Leu Gly Lys Lys Gly Asp Thr Val Glu Leu Thr Cys Thr  
530 535 540

Ala Ser Gln Lys Lys Ser Ile Gln Phe His Trp Lys Asn Ser Asn Gln  
545 550 555 560

Ile Lys Ile Leu Gly Asn Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser  
565 570 575

Lys Leu Asn Asp Arg Ala Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly  
580 585 590

Asn Phe Pro Leu Ile Ile Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr  
595 600 605

Tyr Ile Cys Glu Val Glu Asp Gln Lys Glu Glu Val Gln Leu Leu Val  
610 615 620

Phe Gly Leu Thr Ala Asn Ser Asp Thr His Leu Leu Gln Gly Gln Ser  
625 630 635 640

Leu Thr Leu Thr Leu Glu Ser Pro Pro Gly Ser Ser Pro Ser Val Gln  
645 650 655

Cys Arg Ser Pro Arg Gly Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser  
660 665 670

Val Ser Gln Leu Glu Leu Gln Asp Ser Gly Thr Trp Thr Cys Thr Val  
675 680 685

Leu Gln Asn Gln Lys Lys Val Glu Phe Lys Ile Asp Ile Val Val Leu  
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Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Xaa Tyr Val Xaa Thr  
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tggaaggagg ccaccaccac cctgttctgc gccagcgacc gcaaggccta cgacaccgag 180  
gtgcacaacg tgtggggccac ccacgcctgc gtgcccaccg accccaaccc ccaggaggtg 240  
gagctgaaga acgtgaccga gaacttcaac atgtggaaga acaacatggg ggagcagatg 300  
cacgaggaca tcatcagcct gtgggaccag agcctgaagc cctgcgtgaa gctgaccccc 360  
ctgtgcgtga ccctgaactg caccgacctg cgcaacgcc acaacggcaa cgacaccaac 420  
accactagta gcagccgcgg catggtggggc ggcgggcgaga tgaagaactg cagcttcaac 480  
atcaccacca acatccgcgg caaggtgcag aaggagtacg ccctgttcta caagctggac 540  
atcgccccca tcgacaacaa cagcaacaac cgctaccgcc tgatcagctg caacaccagc 600  
gtgatcacc aggctgccc caaggtgagc ttcgagccca tccccatcca ctactgcgcc 660  
cccgccggct tcgccatcct gaagtgaag gacaagaagt tcaacggcaa gggcccctgc 720  
accaacgtga gcaccgtgca gtgacccac ggcacccgcc ccgtggtgag caccagctg 780  
ctgctgaacg gcagcctggc cgaggaggag gtggtgatcc gcagcgccaa cttcgccgac 840  
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aacaacaaca cccgcaagtc catccacatc ggccccggcc gcgccttcta caccaccggc 960  
gagatcatcg gcgacatccg ccaggcccac tgcaacctga gccgcgccaa gtggaacgac 1020  
accctgaaca agatcgtgat caagctgctg gagcagttcg gcaacaagac catcgtgttc 1080  
aagcacagca gcggcggcga ccccgagatc gtgaccacaca gcttcaattg cggcgggcag 1140  
ttcttctact gcaacagcac ccagctgttc aacagcacct ggaacgtgac cgaggagagc 1200

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aacaacaccg tggagaacaa caccatcacc ctgccctgcc gcatcaagca gatcatcaac 1260
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agttchaaca tcaccggcct gctgctgacc cgcgacggcg gccccgagga caacaagacc 1380
gaggtgttcc gccccggcgg cggcgacatg cgcgacaact ggcgcagcga gctgtacaag 1440
tacaaggtgg tgaagatcga gcccctgggc gtggccccc ccaaggccaa ggcgcgctg 1500
gtgcagcgcg agaagaccgg atcctctggt ggcggtggct cgggctccgg aggaggtggg 1560
tcgggtggcg gcgcggccgc ttgcaacctg gcccgctgcc agctgcgctg caagagcctg 1620
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<210> 6
<211> 556
<212> PRT
<213> Artificial Sequence

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<220>
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<223> X can be any amino acid

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Met Pro Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu Leu Gly
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Met Leu Val Ala Ser Cys Leu Gly Asn Ala Glu Glu Lys Leu Trp Val
          20          25          30

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Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr Thr Leu
          35          40          45

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Phe Cys Ala Ser Asp Arg Lys Ala Tyr Asp Thr Glu Val His Asn Val
          50          55          60

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Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Val
65          70          75          80

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Glu Leu Lys Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met
          85          90          95

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Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu  
100 105 110

Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Thr  
115 120 125

Asp Leu Arg Asn Ala Thr Asn Gly Asn Asp Thr Asn Thr Thr Ser Ser  
130 135 140

Ser Arg Gly Met Val Gly Gly Gly Glu Met Lys Asn Cys Ser Phe Asn  
145 150 155 160

Ile Thr Thr Asn Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Leu Phe  
165 170 175

Tyr Lys Leu Asp Ile Ala Pro Ile Asp Asn Asn Ser Asn Asn Arg Tyr  
180 185 190

Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys  
195 200 205

Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe  
210 215 220

Ala Ile Leu Lys Cys Lys Asp Lys Lys Phe Asn Gly Lys Gly Pro Cys  
225 230 235 240

Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val  
245 250 255

Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val  
260 265 270

Ile Arg Ser Ala Asn Phe Ala Asp Asn Ala Lys Val Ile Ile Val Gln  
275 280 285

Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr  
290 295 300

Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly  
305 310 315 320

Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala  
 325 330 335

Lys Trp Asn Asp Thr Leu Asn Lys Ile Val Ile Lys Leu Arg Glu Gln  
 340 345 350

Phe Gly Asn Lys Thr Ile Val Phe Lys His Ser Ser Gly Gly Asp Pro  
 355 360 365

Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys  
 370 375 380

Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Asn Val Thr Glu Glu Ser  
 385 390 395 400

Asn Asn Thr Val Glu Asn Asn Thr Ile Thr Leu Pro Cys Arg Ile Lys  
 405 410 415

Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala Met Tyr Ala Pro  
 420 425 430

Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu  
 435 440 445

Leu Thr Arg Asp Gly Gly Pro Glu Asp Asn Lys Thr Glu Val Phe Arg  
 450 455 460

Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys  
 465 470 475 480

Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala  
 485 490 495

Lys Arg Arg Val Val Gln Arg Glu Lys Thr Gly Ser Ser Gly Gly Gly  
 500 505 510

Gly Ser Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ala Ala Ala Cys  
 515 520 525

Asn Leu Ala Arg Cys Gln Leu Arg Cys Lys Ser Leu Gly Leu Leu Gly  
 530 535 540

Lys Cys Ala Gly Ser Phe Cys Ala Cys Gly Pro Xaa

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 <211> 66  
 <212> DNA  
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gcgctt 66

<210> 9  
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aaaggggat 69

<210> 10  
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<212> DNA  
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<220>  
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<222> (1)..(76)  
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<210> 11  
<211> 21  
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cagatgcacg aggacatcat cagcctgtgg gaccagagcc tgaagccctg cgtgaagctg 180  
acccccctgt gcgtgaccct gggcgcgggc gagatgaaga actgcagctt caacatcggc 240  
gcgggcccgc tgatcagctg caacaccagc gtgatcacc aggctgccc caaggtgagc 300  
ttcgagccca tccccatcca ctactgcgc cccgcgggct tcgccatcct gaagtgaag 360



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Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro  
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Val Val Ile Arg Ser Ala Asn Phe Ala Asp Asn Ala Lys Val Ile Ile  
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Val Gln Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn  
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Asn Thr Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr

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Thr Gly Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser  
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Arg Ala Lys Trp Asn Asp Thr Leu Asn Lys Ile Val Ile Lys Leu Arg  
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Glu Gln Phe Gly Asn Lys Thr Ile Val Phe Lys His Ser Ser Gly Gly  
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Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe  
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Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala Met Tyr  
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Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu  
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Tyr Lys Tyr Lys Val Val Lys Ile Gly Ser Ser Gly Gly Gly Gly Ser  
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Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ala Ala Ala Lys Lys Val  
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Val Leu Gly Lys Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser  
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Ile Leu Gly Asn Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser Lys Leu  
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Pro Leu Ile Ile Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr Tyr Ile  
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Phe Cys Ala Ser Asp Arg Lys Ala Tyr Asp Thr Glu Val His Asn Val  
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Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Val  
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Glu Leu Lys Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met  
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Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu  
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Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Thr  
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Asp Leu Arg Asn Ala Thr Asn Gly Asn Asp Thr Asn Thr Thr Ser Ser  
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Ser Arg Gly Met Val Gly Gly Gly Glu Met Lys Asn Cys Ser Phe Asn



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145		150		155		160
Ile Thr Thr Asn Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Leu Phe						
	165		170		175	
Tyr Lys Leu Asp Ile Ala Pro Ile Asp Asn Asn Ser Asn Asn Arg Tyr						
	180		185		190	
Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys						
	195		200		205	
Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe						
	210		215		220	
Ala Ile Leu Lys Cys Lys Asp Lys Lys Phe Asn Gly Lys Gly Pro Cys						
	225		230		235	240
Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val						
	245		250		255	
Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val						
	260		265		270	
Ile Arg Ser Ala Asn Phe Ala Asp Asn Ala Lys Val Ile Ile Val Gln						
	275		280		285	
Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr						
	290		295		300	
Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly						
	305		310		315	320
Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala						
	325		330		335	
Lys Trp Asn Asp Thr Leu Asn Lys Ile Val Ile Lys Leu Arg Glu Gln						
	340		345		350	
Phe Gly Asn Lys Thr Ile Val Phe Lys His Ser Ser Gly Gly Asp Pro						
	355		360		365	
Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys						
	370		375		380	

Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Asn Val Thr Glu Glu Ser  
385 390 395 400

Asn Asn Thr Val Glu Asn Asn Thr Ile Thr Leu Pro Cys Arg Ile Lys  
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Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala Met Tyr Ala Pro  
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Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu  
435 440 445

Leu Thr Arg Asp Gly Gly Pro Glu Asp Asn Lys Thr Glu Val Phe Arg  
450 455 460

Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys  
465 470 475 480

Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala  
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Lys Arg Arg Val Val Gln Arg Glu Lys Arg  
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ggctccttct taactaaagg tccatccaag ctgaatgac gcgctgactc aagaagaagc 180  
ctttgggacc aaggaaactt cccctgac atcaagaatc ttaagataga agactcagat 240  
acttacatct gtgaagtgga ggaccagaag gaggaggtgc aattgctagt gttcggattg 300  
actgccaaact ctgacaccca cctgcttcag gggcagagcc tgaccctgac cttggagagc 360  
cccctggta gtagccctc agtgcaatgt aggagtccaa ggggtaaaaa catacagggg 420

gggaagaccc tctccgtgtc tcagctggag ctccaggata gtggcacctg gacatgcact 480  
gtcttcgaga accagaagaa ggtggagttc aaaatagaca tcgtggtgct agct 534

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<211> 178  
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Thr Ala Ser Gln Lys Lys Ser Ile Gln Phe His Trp Lys Asn Ser Asn  
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Gln Ile Lys Ile Leu Gly Asn Gln Gly Ser Phe Leu Thr Lys Gly Pro  
35 40 45

Ser Lys Leu Asn Asp Arg Ala Asp Ser Arg Arg Ser Leu Trp Asp Gln  
50 55 60

Gly Asn Phe Pro Leu Ile Ile Lys Asn Leu Lys Ile Glu Asp Ser Asp  
65 70 75 80

Thr Tyr Ile Cys Glu Val Glu Asp Gln Lys Glu Glu Val Gln Leu Leu  
85 90 95

Val Phe Gly Leu Thr Ala Asn Ser Asp Thr His Leu Leu Gln Gly Gln  
100 105 110

Ser Leu Thr Leu Thr Leu Glu Ser Pro Pro Gly Ser Ser Pro Ser Val  
115 120 125

Gln Cys Arg Ser Pro Arg Gly Lys Asn Ile Gln Gly Gly Lys Thr Leu  
130 135 140

Ser Val Ser Gln Leu Glu Leu Gln Asp Ser Gly Thr Trp Thr Cys Thr  
145 150 155 160

Val Leu Gln Asn Gln Lys Lys Val Glu Phe Lys Ile Asp Ile Val Val  
165 170 175

Leu Ala

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<211> 1128  
<212> DNA  
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cagatgcacg aggacatcat cagcctgtgg gaccagagcc tgaagccctg cgtgaagctg 180  
acccccctgt gcgtgaccct gggcgcgggc gagatgaaga actgcagctt caacatcggc 240  
gcggggccgcc tgatcagctg caacaccagc gtgatcacc aggcctgccc caaggtgagc 300  
ttcgagccca tccccatcca ctactgcgcc cccgcgggct tcgccatcct gaagtgaag 360  
gacaagaagt tcaacggcaa gggccccctgc accaacgtga gcaccgtgca gtgcaccac 420  
ggcatccgcc ccgtggtgag caccagctg ctgctgaacg gcagcctggc cgaggaggag 480  
gtggtgatcc gcagcgccaa cttcgccgac aacgccaagg tgatcatcgt gcagctgaac 540  
gagagcgtgg agatcaactg caccgcccc aacaacaaca cccgcaagtc catccacatc 600  
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tgcaacctga gccgcgcaa gtggaacgac accctgaaca agatcgtgat caagctgcgc 720  
gagcagttcg gcaacaagac catcgtgttc aagcacagca gcggcggcga ccccgagatc 780  
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aacagcacct ggaacgtgac cgaggagagc aacaacaccg tggagaacaa caccatcacc 900  
ctgccctgcc gcatcaagca gatcatcaac atgtggcagg aggtggggcg cgccatgtac 960  
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cgcgacggcg gccccgagga caacaagacc gaggtgttcc gccccggcgg cggcgacatg 1080  
cgcgacaact ggcgcagcga gctgtacaag tacaagggtg tgaagatc 1128

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<212> PRT

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20 25 30

Met Trp Lys Asn Asn Met Val Glu Gln Met His Glu Asp Ile Ile Ser  
35 40 45

Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys  
50 55 60

Val Thr Leu Gly Ala Gly Glu Met Lys Asn Cys Ser Phe Asn Ile Gly  
65 70 75 80

Ala Gly Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys  
85 90 95

Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala  
100 105 110

Gly Phe Ala Ile Leu Lys Cys Lys Asp Lys Lys Phe Asn Gly Lys Gly  
115 120 125

Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro  
130 135 140

Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu  
145 150 155 160

Val Val Ile Arg Ser Ala Asn Phe Ala Asp Asn Ala Lys Val Ile Ile  
165 170 175

Val Gln Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn  
180 185 190

Asn Thr Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr  
195 200 205

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Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr Thr Leu  
35 40 45

Phe Cys Ala Ser Asp Arg Lys Ala Tyr Asp Thr Glu Val His Asn Val  
50 55 60

Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Val  
65 70 75 80

Glu Leu Lys Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met  
85 90 95

Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu  
100 105 110

Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Thr  
115 120 125

Asp Leu Arg Asn Ala Thr Asn Gly Asn Asp Thr Asn Thr Thr Ser Ser  
130 135 140

Ser Arg Gly Met Val Gly Gly Gly Glu Met Lys Asn Cys Ser Phe Asn  
145 150 155 160

Ile Thr Thr Asn Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Leu Phe  
165 170 175

Tyr Lys Leu Asp Ile Ala Pro Ile Asp Asn Asn Ser Asn Asn Arg Tyr  
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Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys  
195 200 205

Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe



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220

Ala Ile Leu Lys Cys Lys Asp Lys Lys Phe Asn Gly Lys Gly Pro Cys  
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Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val  
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Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val  
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Ile Arg Ser Ala Asn Phe Ala Asp Asn Ala Lys Val Ile Ile Val Gln  
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Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr  
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Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly  
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Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala  
 325 330 335

Lys Trp Asn Asp Thr Leu Asn Lys Ile Val Ile Lys Leu Arg Glu Gln  
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Phe Gly Asn Lys Thr Ile Val Phe Lys His Ser Ser Gly Gly Asp Pro  
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Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys  
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Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Asn Val Thr Glu Glu Ser  
 385 390 395 400

Asn Asn Thr Val Glu Asn Asn Thr Ile Thr Leu Pro Cys Arg Ile Lys  
 405 410 415

Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala Met Tyr Ala Pro  
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Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu  
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Leu Thr Arg Asp Gly Gly Pro Glu Asp Asn Lys Thr Glu Val Phe Arg  
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Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys  
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 aacaactaca agaccagcc tccggtgctg gactccgacg gctccttctt cctctacagc 660  
 aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg 720  
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Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
35 40 45

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
50 55 60

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
65 70 75 80

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
85 90 95

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
100 105 110

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
115 120 125

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
130 135 140

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
145 150 155 160

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser  
165 170 175

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 180 185 190

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
 195 200 205

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
 210 215 220

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
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Pro Gly Xaa

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